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Reporting Summary

Nature Research wishes to improve the reproducibility of the work that we publish. This form provides structure for consistency and transparency in reporting. For further information on Nature Research policies, see Authors & Referees and the Editorial Policy Checklist.

Statistical parameters

When statistical analyses are reported, confirm that the following items are present in the relevant location (e.g. figure legend, table legend, main text, or Methods section).

n/a	Confirmed	
☐	☒	The exact sample size (*n*) for each experimental group/condition, given as a discrete number and unit of measurement
☐	☒	An indication of whether measurements were taken from distinct samples or whether the same sample was measured repeatedly
☐	☒	The statistical test(s) used AND whether they are one- or two-sided *Only common tests should be described solely by name; describe more complex techniques in the Methods section.*
☒	☐	A description of all covariates tested
☐	☒	A description of any assumptions or corrections, such as tests of normality and adjustment for multiple comparisons
☐	☒	A full description of the statistics including central tendency (e.g. means) or other basic estimates (e.g. regression coefficient) AND variation (e.g. standard deviation) or associated estimates of uncertainty (e.g. confidence intervals)
☐	☒	For null hypothesis testing, the test statistic (e.g. *F*, *t*, *r*) with confidence intervals, effect sizes, degrees of freedom and *P* value noted *Give P values as exact values whenever suitable.*
☒	☐	For Bayesian analysis, information on the choice of priors and Markov chain Monte Carlo settings
☒	☐	For hierarchical and complex designs, identification of the appropriate level for tests and full reporting of outcomes
☒	☐	Estimates of effect sizes (e.g. Cohen's *d*, Pearson's *r*), indicating how they were calculated
☐	☒	Clearly defined error bars *State explicitly what error bars represent (e.g. SD, SE, CI)*

Our web collection on statistics for biologists may be useful.

Software and code

Policy information about availability of computer code

Data collection	No software was used to collect data.
Data analysis	Random forest classification: randomForestSRC package (version 2.5.1) in R 3.3.2. Whole exome sequencing and variant calling: BWA, GATK, Picard, Varscan2. RNA-sequencing: STAR, Cufflinks HLA-typing and neoantigen predictions: Optitype, VEP, NetMHC, pVAC-seq. Needleman-Wunsch TCRb CDR3 region sequence similarity: Biostrings, NJ, and ggtree packages in R 3.4.3. Flow Cytometry: FlowJo version 10.1 Graphical display: GraphPad Prism version 7.0a Statistical analysis: R 3.3.1 (R Foundation for Statistical Computing, Vienna, Austria).

For manuscripts utilizing custom algorithms or software that are central to the research but not yet described in published literature, software must be made available to editors/reviewers upon request. We strongly encourage code deposition in a community repository (e.g. GitHub). See the Nature Research guidelines for submitting code & software for further information.

Data

Policy information about availability of data

All manuscripts must include a data availability statement. This statement should provide the following information, where applicable:

- Accession codes, unique identifiers, or web links for publicly available datasets
- A list of figures that have associated raw data
- A description of any restrictions on data availability

The data reported are tabulated in the main text and supplemental materials. The raw TCR sequence data have been deposited into the ImmuneACCESS project repository of the Adaptive Biotech database (doi:10.21417/B7BW6X). WES and RNAseq data have been deposited into the Sequence Read Archive (Study SRP136187).

Field-specific reporting

Please select the best fit for your research. If you are not sure, read the appropriate sections before making your selection.

☒ Life sciences ☐ Behavioural & social sciences ☐ Ecological, evolutionary & environmental sciences

For a reference copy of the document with all sections, see nature.com/authors/policies/ReportingSummary-flat.pdf

Life sciences study design

All studies must disclose on these points even when the disclosure is negative.

Sample size	A Phase II clinical trial based on an optimum two-stage Phase II Simon design was used to conduct this pilot study. Ten patients were to be treated in Stage 1; in the absence of abscopal responses, the trial would terminate. With one or more abscopal responses in Stage 1, the trial would proceed to enroll an additional 29 patients: a total of at least 4 abscopal responses (10.25%) were needed to exclude futility.
Data exclusions	No data were excluded.
Replication	In vitro measurements (e.g., measurements of soluble factors in the serum) were performed in duplicate or triplicate with similar results.
Randomization	Randomization is not relevant to our study because the study was not designed to compare two treatment arms. A radiation regimen of 6 Gy X 5 was tested for feasibility and safety during Phase I of the two-stage Simon design. In the absence of grade 4-5 toxicity, the study continued to a radiation regimen of 9.5 Gy X 3 in Phase II.
Blinding	Blinding was not relevant to this study since all patients received treatment and the study was not meant to compare outcome of different treatments.

Reporting for specific materials, systems and methods

Materials & experimental systems

n/a	Involved in the study
☒	☐ Unique biological materials
☐	☒ Antibodies
☒	☐ Eukaryotic cell lines
☒	☐ Palaeontology
☐	☒ Animals and other organisms
☐	☒ Human research participants

Methods

n/a	Involved in the study
☒	☐ ChIP-seq
☐	☒ Flow cytometry
☒	☐ MRI-based neuroimaging

Antibodies

Antibodies used	For immunohistochemistry: Rabbit anti-human PDL-1 (CD274) clone SP142 (PDL1, Spring Biosciences catalog number M4420) was used at 1:50 dilution Rabbit anti-human CD8 clone SP57 (Ventana Medical Systems catalog number 790-4460) was used at 1:100 dilution For flow cytometry: Antibody/dye Fluorochrome - Clone - Manufacturer - Concentration Viability dye eFluor 450 - NA - eBioscience - 1:500 CD4 APC-vio770 M-T466 Miltenyi Biotec 1:50

CD4 PE-Cy7 OKT4 BioLegend 1:100
ICOS PerCP-vio700 REA192 Miltenyi Biotec 1:11
ICOS BUV 395 C398.4A BD Biosciences 1:100
CD127 PE-vio770 MB15-18C9 Miltenyi Biotec 1:100
CD127 BV 785 A019D5 BioLegend 1:20
CD25 Viobright FITC 4E3 Miltenyi Biotec 1:20
CD25 BUV 737 2A3 BD Biosciences 1:20
CD3 APC BW264/56 Miltenyi Biotec 1:20
CD3 APC-vio770 BW264/56 Miltenyi Biotec 1:20
CD8 APC-vio770 BW135/80 Miltenyi Biotec 1:100
CD8 BV 711 RPA-T8 BioLegend 1:20
CD45RA Viogreen T6D11 Miltenyi Biotec 1:20
PD-1 PE-vio770 PD1.3.1.3 Miltenyi Biotec 1:11
TIM-3 Viobright FITC F38-2E2 Miltenyi Biotec 1:20
CCR7 PE REA108 Miltenyi Biotec 1:20
CD16 Viogreen VEP13 Miltenyi Biotec 1:20
CD16 BV 605 3G8 BioLegend 1:20
CD8 PerCP-vio700 BW135/80 Miltenyi Biotec 1:100
CD56 PE-vio770 REA196 Miltenyi Biotec 1:20
CD56 APC HCD56 BioLegend 1:20
NKG2D Viobright FITC BAT221 Miltenyi Biotec 1:20
CD137 (41BB) PE REA765 Miltenyi Biotec 1:50
PD-L1 PerCP-eFluor 710 MIH1 eBioscience 1:20
CD14 PE-vio770 TÜK4 Miltenyi Biotec 1:100
CD19 VioBlue LT19 Miltenyi Biotec 1:100
CD20 VioBlue LT20 Miltenyi Biotec 1:50
CD3 VioBlue BW264/56 Miltenyi Biotec 1:100
CD11b FITC M1/70.15.11.5 Miltenyi Biotec 1:20
HLA-DR APC AC122 Miltenyi Biotec 1:20
CD33 PE AC104.3E3 Miltenyi Biotec 1:100
Ki-67 PerCP-Cy5.5 B56 BD Biosciences 1:40
FoxP3 PE 3G3 Miltenyi Biotec 1:11
FoxP3 Alexa Fluor 488 150D BioLegend 1:20
CTLA-4 PE L3D10 BioLegend 1:20

Validation

The antibodies are commercially available and validated by the manufacturer. We used healthy donors peripheral blood cells to confirm the staining specificity and dilutions for flow cytometry.
For immunohistochemistry a tissue microarray containing placental tissue was used as positive control for PDL-1 staining, and tissue microarray containing lymph node and tonsil tissue was used as positive control for CD8 staining

Animals and other organisms

Policy information about studies involving animals; ARRIVE guidelines recommended for reporting animal research

Laboratory animals

Patient-derived tumor xenografts (PDTX) from freshly resected primary lung tumor were implanted in NOD/SCID/gamma (NOG) female mice (CIEA NOG mouse; NOD.Cg-Prkdcscid Il2rgtm1Sug/JicTac, Taconic Animal Laboratory, Germantown, NY), age 4 to 6 weeks.

Wild animals

The study did not involve wild animals.

Field-collected samples

No field-collected samples were used in this study.

Human research participants

Policy information about studies involving human research participants

Population characteristics

Woman (n=23) and men (n=16) age 48 to 97 with metastatic non-small cell lung cancer and at least 2 distinct measurable metastatic sites, an Eastern Cooperative Oncology Group (ECOG) performance status of 2 or less, and at least one prior therapy.

Recruitment

Patients with metastatic NSCLC who presented at NYU for medical care and fulfilled the eligibility criteria (see online methods) as per approved protocol were offered participation in the study.

Flow Cytometry

Plots

Confirm that:

☒ The axis labels state the marker and fluorochrome used (e.g. CD4-FITC).

☒ The axis scales are clearly visible. Include numbers along axes only for bottom left plot of group (a 'group' is an analysis of identical markers).

☒ All plots are contour plots with outliers or pseudocolor plots.

☒ A numerical value for number of cells or percentage (with statistics) is provided.

Methodology

Sample preparation	See methods
Instrument	Samples were acquired on a MACSquant Analyser 10 (Miltenyi Biotec)
Software	Data was analyzed using the FlowJo software version 10.1 (Treestar).
Cell population abundance	Not applicable.
Gating strategy	Gating strategy is illustrated in Supplementary Figure 6.

☒ Tick this box to confirm that a figure exemplifying the gating strategy is provided in the Supplementary Information.